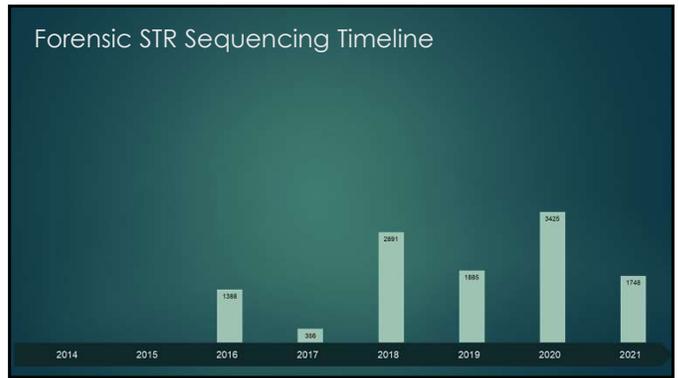
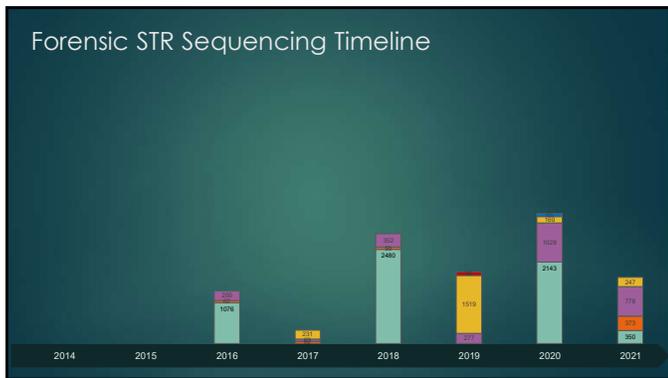


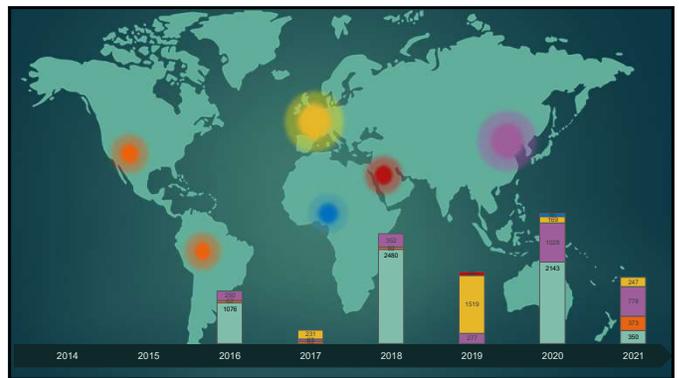
7



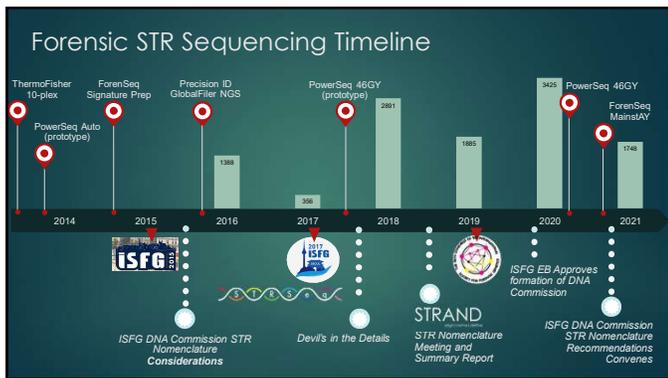
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2016 ISFG DNA Commission STR Sequence Nomenclature Considerations

2019 STRAND WG Meeting

2020 STRAND WG Initiates ISFG DNA Commission STR Sequence Nomenclature Recommendations

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ISFG DNA Commission on STR Sequence Nomenclature

2016 Consideration

- Software that allows STR sequences to be exported and stored in databases as sequence strings
- The forward strand direction can be used to align STR sequences
- GRCh38 is recommended as the framework. Continued discussions are necessary to decide whether or not to adapt to novel genome assemblies
- Translate the nomenclature of reverse strand loci and repeat region start and end points.
- STR sequence strings should include flanking sequences as well as the genome coordinates of the sequence
- Comprehensive STR nomenclature systems are preferred for early adopters. Backward compatibility
- Updated allele frequency databases will be necessary
- Future forensic MPS multiplexes would benefit from retention of past markers

2021 Recommendation

- STRINGS**
Sequenced STR alleles should be maintained as sequence strings oriented to the forward strand of the current genome assembly. Sequences should include the minimum genomic coordinate range described herein, which is designed to provide sufficient flanking region to distinguish the termini of the repeat region.
- BRACKETED REPEAT**
Connections between length and seq representation. Universal parameters for all loci or only new loci
- RESOURCES**
- NEW LOCI**

NIJ Funding

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NIJ Award for STR Nomenclature Resources

Existing Forensic STR Loci

- Update **STRSeq BioProject** Records to match ISFG Recommendations
- Expand Capability of **STRIDER** for STR Sequence-Based Frequencies
- Develop tool allowing users to format strings and link to resources

New STR Loci

- Align historical STR names to modern reference sequence
- Catalog exemplar sequences for new loci

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BioProject Structure

Links to BioProjects

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Record Structure

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Record Structure

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STRIDER MPS Dataset QC

July 2017 - December 2021

STRIDER MPS Dataset QC
Total submissions: 31
Total n = 8,576

Passed QC: 23
Mean n = 277/dataset

Withdrawal during QC: 7

Rejected: 1

NIJ FUNDS will support expanding STRIDER WEBSITE to provide SEQUENCE-BASED STR ALLELE FREQUENCIES

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Thank You!

STRAND Working Group
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**ISFC Executive Board & DNA Commission
on STR Nomenclature Recommendations**

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Funding Sources
NIST Special Programs Office
NIJ Interagency Agreement

